

SEQUENCE LISTING

<110> Reppert, Steven M.
Ebisawa, Takashi

<120> HIGH-AFFINITY MELATONIN RECEPTOR AND USES THEREOF

<130> 10217/250003

<140> US 09/226,046
<141> 1999-01-03

<150> US 08/466,103
<151> 1995-06-06

<150> US 08/319,887
<151> 1994-10-07

<150> US 08/261,857
<151> 1994-06-17

<160> 29

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 1320
<212> DNA
<213> Xenopus laevis

<220>
<221> CDS
<222> (32)...(1291)

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1 5

tgc ttg gat tgc agg aca cct ggt acc ata cga aca gag cag gat gca 100
Cys Leu Asp Cys Arg Thr Pro Gly Thr Ile Arg Thr Glu Gln Asp Ala
10 15 20

cag gac agc gca tct cag gga ctc acc tct gcc ctg gcg gtg gtt ctt 148
Gln Asp Ser Ala Ser Gln Gly Leu Thr Ser Ala Leu Ala Val Val Leu
25 30 35

ata ttc acc att gtt gtg gat gtc ctg ggc aat ata ttg gtc att ttg 196
Ile Phe Thr Ile Val Val Asp Val Leu Gly Asn Ile Leu Val Ile Leu
40 45 50 55

tct gtc ctg agg aac aag aag ctg cag aat gct gga aat ctc ttt gtt 244
Ser Val Leu Arg Asn Lys Lys Leu Gln Asn Ala Gly Asn Leu Phe Val
60 65 70

gtc agt ttg tct att gcc gat ctg gtt gtt gct gtg tat ccc tat ccg 292
Val Ser Leu Ser Ile Ala Asp Leu Val Val Ala Val Tyr Pro Tyr Pro
75 80 85

gtc att ctc ata gct att ttc cag aat gga tgg acg ctt gga aat atc 340
Val Ile Leu Ile Ala Ile Phe Gln Asn Gly Trp Thr Leu Gly Asn Ile
90 95 100

cat tgt cag atc agt ggc ttc ctg atg gga ctc agc gtt att gga tca His Cys Gln Ile Ser Gly Phe Leu Met Gly Leu Ser Val Ile Gly Ser 105 110 115	388
gtc ttc aac ata aca gcc ata gct atc aac agg tat tgc tac atc tgc Val Phe Asn Ile Thr Ala Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys 120 125 130 135	436
cac agc ctg aga tat gac aag ctt tat aat caa aga agc acc tgg tgc His Ser Leu Arg Tyr Asp Lys Leu Tyr Asn Gln Arg Ser Thr Trp Cys 140 145 150	484
tac ctt ggc ctg aca tgg ata cta act ata att gca atc gtg cca aac Tyr Leu Gly Leu Thr Trp Ile Leu Thr Ile Ile Ala Ile Val Pro Asn 155 160 165	532
ttt ttt gtt gga tca cta cag tat gac ccc agg att ttt tct tgc aca Phe Phe Val Gly Ser Leu Gln Tyr Asp Pro Arg Ile Phe Ser Cys Thr 170 175 180	580
ttt gcg cag aca gtg agt tcc tca tac acc ata aca gta gtg gtg gtg Phe Ala Gln Thr Val Ser Ser Ser Tyr Thr Ile Thr Val Val Val Val 185 190 195	628
cat ttt ata gtc cct ctt agt gtt gtg aca ttc tgt tac tta aga ata His Phe Ile Val Pro Leu Ser Val Val Thr Phe Cys Tyr Leu Arg Ile 200 205 210 215	676
tgg gtt tta gtg atc caa gtc aaa cac aga gtt aga caa gac ttc aag Trp Val Leu Val Ile Gln Val Lys His Arg Val Arg Gln Asp Phe Lys 220 225 230	724
caa aag ttg aca caa aca gac ttg aga aat ttc ttg acc atg ttt gtg Gln Lys Leu Thr Gln Thr Asp Leu Arg Asn Phe Leu Thr Met Phe Val 235 240 245	772
gtc ttt gta ctt ttt gca gtt tgc tgg gcc ccc tta aac ttt atc ggc Val Phe Val Leu Phe Ala Val Cys Trp Ala Pro Leu Asn Phe Ile Gly 250 255 260	820
ctt gct gtg gcc att aat ccg ttt cat gtg gca cca aag att cca gaa Leu Ala Val Ala Ile Asn Pro Phe His Val Ala Pro Lys Ile Pro Glu 265 270 275	868
tgg ctg ttt gtt tta agc tat ttc atg gcc tat ttt aac agt tgt ctc Trp Leu Phe Val Leu Ser Tyr Phe Met Ala Tyr Phe Asn Ser Cys Leu 280 285 290 295	916
aat gct gtt ata tat ggt gtg cta aat caa aac ttc cgc aag gag tac Asn Ala Val Ile Tyr Gly Val Leu Asn Gln Asn Phe Arg Lys Glu Tyr 300 305 310	964
aaa aga ata ctg atg tcc tta ttg act cca aga ctg ttg ttt ctt gac Lys Arg Ile Leu Met Ser Leu Leu Thr Pro Arg Leu Leu Phe Leu Asp 315 320 325	1012
aca tct aga gga gga act gag gga ttg aaa agt aag cct tcg cca gct Thr Ser Arg Gly Gly Thr Glu Gly Leu Lys Ser Lys Pro Ser Pro Ala 330 335 340	1060

gta acc aac aac aat caa gca gat atg cta gga gaa gca agg tca ctg 1108
Val Thr Asn Asn Asn Gln Ala Asp Met Leu Gly Glu Ala Arg Ser Leu 355
345 350

tgg ctg agc agg aga aat ggt gcg aaa atg gtg atc atc atc agg cca 1156
Trp Leu Ser Arg Arg Asn Gly Ala Lys Met Val Ile Ile Ile Arg Pro 375
360 365 370

aga aaa gca caa att gca atc atc cat caa ata ttc tgg cct cag agt 1204
Arg Lys Ala Gln Ile Ala Ile Ile His Gln Ile Phe Trp Pro Gln Ser 390
380 385

tca tgg gca aca tgc cgt caa gac aca aag att acc gga gaa gaa gat 1252
Ser Trp Ala Thr Cys Arg Gln Asp Thr Lys Ile Thr Gly Glu Glu Asp 405
395 400

ggc tgc cgt gaa ctg tgc aag gac ggg att tcc caa agg tgagacccaa 1301
Gly Cys Arg Glu Leu Cys Lys Asp Gly Ile Ser Gln Arg 420
410 415

1320

tgcaactatat ccacattat

<210> 2
<211> 420
<212> PRT
<213> Xenopus laevis

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Ile Arg Thr Glu Gln Asp Ala Gln Asp Ser Ala Ser Gln Gly Leu Thr 30
20 25
Ser Ala Leu Ala Val Val Leu Ile Phe Thr Ile Val Val Asp Val Leu 45
35 40
Gly Asn Ile Leu Val Ile Leu Ser Val Leu Arg Asn Lys Lys Leu Gln 60
50 55
Asn Ala Gly Asn Leu Phe Val Val Ser Leu Ser Ile Ala Asp Leu Val 80
65 70 75
Val Ala Val Tyr Pro Tyr Pro Val Ile Leu Ile Ala Ile Phe Gln Asn 95
85 90
Gly Trp Thr Leu Gly Asn Ile His Cys Gln Ile Ser Gly Phe Leu Met 110
100 105
Gly Leu Ser Val Ile Gly Ser Val Phe Asn Ile Thr Ala Ile Ala Ile 125
115 120
Asn Arg Tyr Cys Tyr Ile Cys His Ser Leu Arg Tyr Asp Lys Leu Tyr 140
130 135
Asn Gln Arg Ser Thr Trp Cys Tyr Leu Gly Leu Thr Trp Ile Leu Thr 160
145 150 155
Ile Ile Ala Ile Val Pro Asn Phe Phe Val Gly Ser Leu Gln Tyr Asp 175
165 170
Pro Arg Ile Phe Ser Cys Thr Phe Ala Gln Thr Val Ser Ser Ser Tyr 190
180 185
Thr Ile Thr Val Val Val Val His Phe Ile Val Pro Leu Ser Val Val 205
195 200
Thr Phe Cys Tyr Leu Arg Ile Trp Val Leu Val Ile Gln Val Lys His 220
210 215
Arg Val Arg Gln Asp Phe Lys Gln Lys Leu Thr Gln Thr Asp Leu Arg 240
225 230 235
Asn Phe Leu Thr Met Phe Val Val Phe Val Leu Phe Ala Val Cys Trp 255
245 250
Ala Pro Leu Asn Phe Ile Gly Leu Ala Val Ala Ile Asn Pro Phe His 270
260 265

Val Ala Pro Lys Ile Pro Glu Trp Leu Phe Val Leu Ser Tyr Phe Met
 275 280 285
 Ala Tyr Phe Asn Ser Cys Leu Asn Ala Val Ile Tyr Gly Val Leu Asn
 290 295 300
 Gln Asn Phe Arg Lys Glu Tyr Lys Arg Ile Leu Met Ser Leu Leu Thr
 305 310 315 320
 Pro Arg Leu Leu Phe Leu Asp Thr Ser Arg Gly Gly Thr Glu Gly Leu
 325 330 335
 Lys Ser Lys Pro Ser Pro Ala Val Thr Asn Asn Asn Gln Ala Asp Met
 340 345 350
 Leu Gly Glu Ala Arg Ser Leu Trp Leu Ser Arg Arg Asn Gly Ala Lys
 355 360 365
 Met Val Ile Ile Ile Arg Pro Arg Lys Ala Gln Ile Ala Ile Ile His
 370 375 380
 Gln Ile Phe Trp Pro Gln Ser Ser Trp Ala Thr Cys Arg Gln Asp Thr
 385 390 395 400
 Lys Ile Thr Gly Glu Glu Asp Gly Cys Arg Glu Leu Cys Lys Asp Gly
 405 410 415
 Ile Ser Gln Arg
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<210> 3
 <211> 1149
 <212> DNA
 <213> Ovis
 <220>
 <221> CDS
 <222> (49)...(1146)

<400> 3
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 Met Ala Gly
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cgg ctg tgg ggc tgc ccg ggc ggg acc ccc aag ggc aac ggc agc agc
 Arg Leu Trp Gly Ser Pro Gly Gly Thr Pro Lys Gly Asn Gly Ser Ser
 5 10 15

gcg ctg ctc aac gtc tgc cag gcg gcg ccc ggc gcc ggg gac ggt gtg
 Ala Leu Leu Asn Val Ser Gln Ala Ala Pro Gly Ala Gly Asp Gly Val
 20 25 30 35

cgg ccg cgg ccc tgc tgg ctg gcc gcc acc ctc gcc tcc atc ctc atc
 Arg Pro Arg Pro Ser Trp Leu Ala Ala Thr Leu Ala Ser Ile Leu Ile
 40 45 50

ttc acc atc gtg gtg gac atc gtg ggc aac ctc ctg gtg gtc ctg tcc
 Phe Thr Ile Val Val Asp Ile Val Gly Asn Leu Leu Val Val Leu Ser
 55 60 65

gtg tat cgg aac aag aag ctg agg aac gca ggg aat gtg ttt gtg gtg
 Val Tyr Arg Asn Lys Lys Leu Arg Asn Ala Gly Asn Val Phe Val Val
 70 75 80

agc ctg gca gtt gca gac ctg ctg gtg gcc gtg tat ccg tac ccc ttg
 Ser Leu Ala Val Ala Asp Leu Leu Val Ala Val Tyr Pro Tyr Pro Leu
 85 90 95

gcg ctg gcg tct ata gtt aac aat ggg tgg agc ctg agc tcc ctg cat
 Ala Leu Ala Ser Ile Val Asn Asn Gly Trp Ser Leu Ser Ser Leu His
 100 105 110 115

tgc caa ctt agt ggc ttc ctg atg ggc ttg agc gtc atc ggg tcc gtt Cys Gln Leu Ser Gly Phe Leu Met Gly Leu Ser Val Ile Gly Ser Val 120 125 130	441
ttc agc atc acg gga att gcc atc aac cgc tat tgc tgc atc tgc cac Phe Ser Ile Thr Gly Ile Ala Ile Asn Arg Tyr Cys Cys Ile Cys His 135 140 145	489
agc ctc aga tac ggc aag ctg tat agc ggc acg aat tcc ctc tgc tac Ser Leu Arg Tyr Gly Lys Leu Tyr Ser Gly Thr Asn Ser Leu Cys Tyr 150 155 160	537
gtg ttc ctg atc tgg acg ctg acg ctc gtg gcg atc gtg ccc aac ctg Val Phe Leu Ile Trp Thr Leu Thr Leu Val Ala Ile Val Pro Asn Leu 165 170 175	585
tgt gtg ggg acc ctg cag tac gac ccg agg atc tat tcc tgt acc ttc Cys Val Gly Thr Leu Gln Tyr Asp Pro Arg Ile Tyr Ser Cys Thr Phe 180 185 190 195	633
acg cag tcc gtc agc tca gcc tac acg atc gcc gtg gtg gtg ttc cat Thr Gln Ser Val Ser Ser Ala Tyr Thr Ile Ala Val Val Val Phe His 200 205 210	681
ttc ata gtt ccg atg ctc gta gtc gtc ttc tgt tac ctg aga atc tgg Phe Ile Val Pro Met Leu Val Val Val Phe Cys Tyr Leu Arg Ile Trp 215 220 225	729
gcc ctg gtt ctt cag gtc aga tgg aag gtg aaa ccg gac aac aaa ccg Ala Leu Val Leu Gln Val Arg Trp Lys Val Lys Pro Asp Asn Lys Pro 230 235 240	777
aaa ctg aag ccc cag gac ttc agg aat ttt gtc acc atg ttt gtg gtt Lys Leu Lys Pro Gln Asp Phe Arg Asn Phe Val Thr Met Phe Val Val 245 250 255	825
ttt gtc ctc ttt gcc att tgc tgg gct cct ctg aac ttc att ggt ctc Phe Val Leu Phe Ala Ile Cys Trp Ala Pro Leu Asn Phe Ile Gly Leu 260 265 270 275	873
gtt gtg gcc tcg gac ccc gcc agc atg gca ccc agg atc ccc gag tgg Val Val Ala Ser Asp Pro Ala Ser Met Ala Pro Arg Ile Pro Glu Trp 280 285 290	921
ctg ttt gtg gct agt tac tat atg gca tat ttc aac agc tgc ctc aat Leu Phe Val Ala Ser Tyr Tyr Met Ala Tyr Phe Asn Ser Cys Leu Asn 295 300 305	969
gcg atc ata tat gga cta ctg aac caa aat ttc agg cag gaa tac aga Ala Ile Ile Tyr Gly Leu Leu Asn Gln Asn Phe Arg Gln Glu Tyr Arg 310 315 320	1017
aaa att ata gtc tca ttg tgt acc acc aag atg ttc ttt gtg gat agc Lys Ile Ile Val Ser Leu Cys Thr Thr Lys Met Phe Phe Val Asp Ser 325 330 335	1065
tcc aat cat gta gca gat aga att aaa cgc aaa ccc tct cca tta ata Ser Asn His Val Ala Asp Arg Ile Lys Arg Lys Pro Ser Pro Leu Ile 340 345 350 355	1113

gcc aac cat aac cta ata aag gtg gac tcc gtt taa
 Ala Asn His Asn Leu Ile Lys Val Asp Ser Val
 360 365

1149

<210> 4
 <211> 366
 <212> PRT
 <213> Ovis

<400> 4
 Met Ala Gly Arg Leu Trp Gly Ser Pro Gly Gly Thr Pro Lys Gly Asn
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 20 25 30
 Asp Gly Val Arg Pro Arg Pro Ser Trp Leu Ala Ala Thr Leu Ala Ser
 35 40 45
 Ile Leu Ile Phe Thr Ile Val Val Asp Ile Val Gly Asn Leu Leu Val
 50 55 60
 Val Leu Ser Val Tyr Arg Asn Lys Lys Leu Arg Asn Ala Gly Asn Val
 65 70 75 80
 Phe Val Val Ser Leu Ala Val Ala Asp Leu Leu Val Ala Val Tyr Pro
 85 90 95
 Tyr Pro Leu Ala Leu Ala Ser Ile Val Asn Asn Gly Trp Ser Leu Ser
 100 105 110
 Ser Leu His Cys Gln Leu Ser Gly Phe Leu Met Gly Leu Ser Val Ile
 115 120 125
 Gly Ser Val Phe Ser Ile Thr Gly Ile Ala Ile Asn Arg Tyr Cys Cys
 130 135 140
 Ile Cys His Ser Leu Arg Tyr Gly Lys Leu Tyr Ser Gly Thr Asn Ser
 145 150 155 160
 Leu Cys Tyr Val Phe Leu Ile Trp Thr Leu Val Ala Ile Val
 165 170 175
 Pro Asn Leu Cys Val Gly Thr Leu Gln Tyr Asp Pro Arg Ile Tyr Ser
 180 185 190
 Cys Thr Phe Thr Gln Ser Val Ser Ser Ala Tyr Thr Ile Ala Val Val
 195 200 205
 Val Phe His Phe Ile Val Pro Met Leu Val Val Val Phe Cys Tyr Leu
 210 215 220
 Arg Ile Trp Ala Leu Val Leu Gln Val Arg Trp Lys Val Lys Pro Asp
 225 230 235 240
 Asn Lys Pro Lys Leu Lys Pro Gln Asp Phe Arg Asn Phe Val Thr Met
 245 250 255
 Phe Val Val Phe Val Leu Phe Ala Ile Cys Trp Ala Pro Leu Asn Phe
 260 265 270
 Ile Gly Leu Val Val Ala Ser Asp Pro Ala Ser Met Ala Pro Arg Ile
 275 280 285
 Pro Glu Trp Leu Phe Val Ala Ser Tyr Tyr Met Ala Tyr Phe Asn Ser
 290 295 300
 Cys Leu Asn Ala Ile Ile Tyr Gly Leu Leu Asn Gln Asn Phe Arg Gln
 305 310 315 320
 Glu Tyr Arg Lys Ile Ile Val Ser Leu Cys Thr Thr Lys Met Phe Phe
 325 330 335
 Val Asp Ser Ser Asn His Val Ala Asp Arg Ile Lys Arg Lys Pro Ser
 340 345 350
 Pro Leu Ile Ala Asn His Asn Leu Ile Lys Val Asp Ser Val
 355 360 365

<210> 5
 <211> 867
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(864)

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att tat ccg tac ccg ttg gtg ctg atg tgc ata ttt aac aac ggg tgg Ile Tyr Pro Tyr Pro Leu Val Leu Met Ser Ile Phe Asn Asn Gly Trp 20 25 30	96
aac ctg ggc tat ctg cac tgc caa gtc agt ggg ttc ctg atg ggc ctg Asn Leu Gly Tyr Leu His Cys Gln Val Ser Gly Phe Leu Met Gly Leu 35 40 45	144
agc gtc atc ggc tcc ata ttc aac atc acc ggc atc gcc atc aac cgc Ser Val Ile Gly Ser Ile Phe Asn Ile Thr Gly Ile Ala Ile Asn Arg 50 55 60	192
tac tgt tac atc tgc cac agt ctc aag tgc gac aaa ctg tac agc agc Tyr Cys Tyr Ile Cys His Ser Leu Lys Cys Asp Lys Leu Tyr Ser Ser 65 70 75 80	240
aag aac tcc ctc tgc tac gtg ctc ctc ata tgg ctc ctg acg gcg gcc Lys Asn Ser Leu Cys Tyr Val Leu Leu Ile Trp Leu Leu Thr Ala Ala 85 90 95	288
gtc ctg ccc aac ctc cgt cgt ggg act ctc cag tac gag ccg agg atc Val Leu Pro Asn Leu Arg Arg Gly Thr Leu Gln Tyr Glu Pro Arg Ile 100 105 110	336
tac tgc tgc acc ttc gcc cag tcc gtc agc tcc gcc tac acc atc gcc Tyr Ser Cys Thr Phe Ala Gln Ser Val Ser Ser Ala Tyr Thr Ile Ala 115 120 125	384
gtg gtg gtt ttc cac ttc ctc gtc ccc atg atc ata gtc atc ttc tgt Val Val Val Phe His Phe Leu Val Pro Met Ile Ile Val Ile Phe Cys 130 135 140	432
tac ctg aga ata tgg atc ctg gtt ctc cag gtc aga cag agg gtg aaa Tyr Leu Arg Ile Trp Ile Leu Val Leu Gln Val Arg Gln Arg Val Lys 145 150 155 160	480
cct gac cgc aaa ccc aaa ctg aaa cca cac gac ttc agg aat ttt gtc Pro Asp Arg Lys Pro Lys Leu Lys Pro His Asp Phe Arg Asn Phe Val 165 170 175	528
acc atg ttt gtg gtt ttt gtc ctt ttt gcc att tgc tgg gct cct ctg Thr Met Phe Val Val Phe Val Leu Phe Ala Ile Cys Trp Ala Pro Leu 180 185 190	576
aac ttc att ggc ctg gcc gtg gcc tct gac ccc gcc agc atg gtg cct Asn Phe Ile Gly Leu Ala Val Ala Ser Asp Pro Ala Ser Met Val Pro 195 200 205	624
agg atc cca gag tgg ctg ttt gtg gcc agt tac tac atg gcg tat ttc Arg Ile Pro Glu Trp Leu Phe Val Ala Ser Tyr Tyr Met Ala Tyr Phe 210 215 220	672

aac agc tgc ctc aat gcc att ata tcg ggc tac tgg aac caa aat ttc 720
 Asn Ser Cys Leu Asn Ala Ile Ile Ser Gly Tyr Trp Asn Gln Asn Phe 240
 225 230 235
 agg aag gaa tac agg aga att ata gtc tcg ctc gtg aca gcc agg gtg 768
 Arg Lys Glu Tyr Arg Arg Ile Ile Val Ser Leu Val Thr Ala Arg Val 255
 245 250
 ttc ttt gtg gac agc tct aac gac gtg gcc gat agg gtt aaa tgg aaa 816
 Phe Phe Val Asp Ser Ser Asn Asp Val Ala Asp Arg Val Lys Trp Lys 270
 260 265
 ccg tct cca ctg atg acc aac aat aat gta gta aag gtg gac tcc gtt 864
 Pro Ser Pro Leu Met Thr Asn Asn Asn Val Val Lys Val Asp Ser Val 285
 275 280
 taa 867

<210> 6
 <211> 288
 <212> PRT
 <213> Homo sapiens

<400> 6
 Gly Asn Ile Phe Val Val Ser Leu Ala Val Ala Asp Leu Val Val Ala 15
 1 5 10
 Ile Tyr Pro Tyr Pro Leu Val Leu Met Ser Ile Phe Asn Asn Gly Trp 30
 20 25
 Asn Leu Gly Tyr Leu His Cys Gln Val Ser Gly Phe Leu Met Gly Leu 45
 35 40
 Ser Val Ile Gly Ser Ile Phe Asn Ile Thr Gly Ile Ala Ile Asn Arg 60
 50 55
 Tyr Cys Tyr Ile Cys His Ser Leu Lys Cys Asp Lys Leu Tyr Ser Ser 80
 65 70 75
 Lys Asn Ser Leu Cys Tyr Val Leu Leu Ile Trp Leu Leu Thr Ala Ala 95
 85 90
 Val Leu Pro Asn Leu Arg Arg Gly Thr Leu Gln Tyr Glu Pro Arg Ile 110
 100 105
 Tyr Ser Cys Thr Phe Ala Gln Ser Val Ser Ser Ala Tyr Thr Ile Ala 125
 115 120
 Val Val Val Phe His Phe Leu Val Pro Met Ile Ile Val Ile Phe Cys 140
 130 135
 Tyr Leu Arg Ile Trp Ile Leu Val Leu Gln Val Arg Gln Arg Val Lys 160
 145 150
 Pro Asp Arg Lys Pro Lys Leu Lys Pro His Asp Phe Arg Asn Phe Val 175
 165 170
 Thr Met Phe Val Val Phe Val Leu Phe Ala Ile Cys Trp Ala Pro Leu 190
 180 185
 Asn Phe Ile Gly Leu Ala Val Ala Ser Asp Pro Ala Ser Met Val Pro 205
 195 200
 Arg Ile Pro Glu Trp Leu Phe Val Ala Ser Tyr Tyr Met Ala Tyr Phe 220
 210 215
 Asn Ser Cys Leu Asn Ala Ile Ile Ser Gly Tyr Trp Asn Gln Asn Phe 240
 225 230 235
 Arg Lys Glu Tyr Arg Arg Ile Ile Val Ser Leu Val Thr Ala Arg Val 255
 245 250
 Phe Phe Val Asp Ser Ser Asn Asp Val Ala Asp Arg Val Lys Trp Lys 270
 260 265
 Pro Ser Pro Leu Met Thr Asn Asn Asn Val Val Lys Val Asp Ser Val 285
 275 280

<210> 7
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 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(5)
 <223> Xaa = Any Amino Acid

<400> 7
 Asn Pro Xaa Xaa Tyr
 1 5

<210> 8
 <211> 7
 <212> PRT
 <213> Xenopus laevis

<400> 8
 Ala Ile Ala Ile Asn Arg Tyr
 1 5

<210> 9
 <211> 8
 <212> PRT
 <213> Xenopus laevis

<400> 9
 Phe Ala Val Cys Trp Ala Pro Leu
 1 5

<210> 10
 <211> 6
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(6)
 <223> Xaa = Any Amino Acid

<400> 10
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 1 5

<210> 11
 <211> 1085
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (33)...(1082)

<400> 11
 atggccctgc ggccgggacg cgaacaggga cc atg cag ggc aac ggc agc gcg
 Met Gln Gly Asn Gly Ser Ala
 1 5

53

ctg ccc aac gcc tcc cag ccc gtg ctc cgc ggg gac ggc gcg cgg ccc 101
 Leu Pro Asn Ala Ser Gln Pro Val Leu Arg Gly Asp Gly Ala Arg Pro 20
 10

tcg tgg ctg gcg tcc gcc cta gcc tgc gtc ctc atc ttc acc atc gtg 149
 Ser Trp Leu Ala Ser Ala Leu Ala Cys Val Leu Ile Phe Thr Ile Val 35
 25

gtg gac atc ctg ggc aac ctc ctg gtc atc ctg tgc gtg tat cgg aac 197
 Val Asp Ile Leu Gly Asn Leu Leu Val Ile Leu Ser Val Tyr Arg Asn 55
 40

aag aag ctc agg aac gca gga aac atc ttt gtg gtg agc tta gcg gtg 245
 Lys Lys Leu Arg Asn Ala Gly Asn Ile Phe Val Val Ser Leu Ala Val 70
 60

gca gac ctg gtg gtg gcc att tat ccg tac ccg ttg gtg ctg atg tgc 293
 Ala Asp Leu Val Val Ala Ile Tyr Pro Tyr Pro Leu Val Leu Met Ser 85
 75

ata ttt aac aac ggg tgg aac ctg ggc tat ctg cac tgc caa gtc agt 341
 Ile Phe Asn Asn Gly Trp Asn Leu Gly Tyr Leu His Cys Gln Val Ser 100
 90

ggg ttc ctg atg ggc ctg agc gtc atc ggc tcc ata ttc aac atc acc 389
 Gly Phe Leu Met Gly Leu Ser Val Ile Gly Ser Ile Phe Asn Ile Thr 115
 105

ggc atc gcc atc aac cgc tac tgc tac atc tgc cac agt ctc aag tac 437
 Gly Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys His Ser Leu Lys Tyr 135
 120

gac aaa ctg tac agc agc aag aac tcc ctc tgc tac gtg ctc ctc ata 485
 Asp Lys Leu Tyr Ser Ser Lys Asn Ser Leu Cys Tyr Val Leu Leu Ile 150
 140

tgg ctc ctg acg ctg gcg gcc gtc ctg ccc aac ctc cgt gca ggg act 533
 Trp Leu Leu Thr Leu Ala Ala Val Leu Pro Asn Leu Arg Ala Gly Thr 165
 155

ctc cag tac gac ccg agg atc tac tgc tgc acc ttc gcc cag tcc gtc 581
 Leu Gln Tyr Asp Pro Arg Ile Tyr Ser Cys Thr Phe Ala Gln Ser Val 180
 170

agc tcc gcc tac acc atc gcc gtg gtg gtt ttc cac ttc ctc gtc ccc 629
 Ser Ser Ala Tyr Thr Ile Ala Val Val Val Phe His Phe Leu Val Pro 195
 185

atg atc ata gtc atc ttc tgt tac ctg aga ata tgg atc ctg gtt ctc 677
 Met Ile Ile Val Ile Phe Cys Tyr Leu Arg Ile Trp Ile Leu Val Leu 215
 200

cag gtc aga cag agg gtg aaa cct gac cgc aaa ccc aaa ctg aaa cca 725
 Gln Val Arg Gln Arg Val Lys Pro Asp Arg Lys Pro Lys Leu Lys Pro 230
 220

cag gac ttc agg aat ttt gtc acc atg ttt gtg gtt ttt gtc ctc ttt 773
 Gln Asp Phe Arg Asn Phe Val Thr Met Phe Val Val Phe Val Leu Phe 245
 235

gcc att tgc tgg gct cct ctg aac ttc att ggc ctg gcc gtg gcc tct	821
Ala Ile Cys Trp Ala Pro Leu Asn Phe Ile Gly Leu Ala Val Ala Ser	
250 255 260	
gac ccc gcc agc atg gtg cct agg atc cca gag tgg ctg ttt gtg gcc	869
Asp Pro Ala Ser Met Val Pro Arg Ile Pro Glu Trp Leu Phe Val Ala	
265 270 275	
agt tac tac atg gcg tat ttc aac agc tgc ctc aat gcc att ata tac	917
Ser Tyr Tyr Met Ala Tyr Phe Asn Ser Cys Leu Asn Ala Ile Ile Tyr	
280 285 290 295	
ggg cta ctg aac caa aat ttc agg aag gaa tac agg aga att ata gtc	965
Gly Leu Leu Asn Gln Asn Phe Arg Lys Glu Tyr Arg Arg Ile Ile Val	
300 305 310	
tcg ctc tgt aca gcc agg gtg ttc ttt gtg gac agc tct aac gac gtg	1013
Ser Leu Cys Thr Ala Arg Val Phe Phe Val Asp Ser Ser Asn Asp Val	
315 320 325	
gcc gat agg gtt aaa tgg aaa ccg tct cca ctg atg acc aac aat aat	1061
Ala Asp Arg Val Lys Trp Lys Pro Ser Pro Leu Met Thr Asn Asn Asn	
330 335 340	
gta gta aag gtg gac tcc gtt taa	1085
Val Val Lys Val Asp Ser Val	
345 350	

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<400> 12

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Arg Gly Asp Gly Ala Arg Pro Ser Trp Leu Ala Ser Ala Leu Ala Cys	
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Val Leu Ile Phe Thr Ile Val Val Asp Ile Leu Gly Asn Leu Leu Val	
35 40 45	
Ile Leu Ser Val Tyr Arg Asn Lys Lys Leu Arg Asn Ala Gly Asn Ile	
50 55 60	
Phe Val Val Ser Leu Ala Val Ala Asp Leu Val Val Ala Ile Tyr Pro	
65 70 75 80	
Tyr Pro Leu Val Leu Met Ser Ile Phe Asn Asn Gly Trp Asn Leu Gly	
85 90 95	
Tyr Leu His Cys Gln Val Ser Gly Phe Leu Met Gly Leu Ser Val Ile	
100 105 110	
Gly Ser Ile Phe Asn Ile Thr Gly Ile Ala Ile Asn Arg Tyr Cys Tyr	
115 120 125	
Ile Cys His Ser Leu Lys Tyr Asp Lys Leu Tyr Ser Ser Lys Asn Ser	
130 135 140	
Leu Cys Tyr Val Leu Leu Ile Trp Leu Leu Thr Leu Ala Ala Val Leu	
145 150 155 160	
Pro Asn Leu Arg Ala Gly Thr Leu Gln Tyr Asp Pro Arg Ile Tyr Ser	
165 170 175	
Cys Thr Phe Ala Gln Ser Val Ser Ser Ala Tyr Thr Ile Ala Val Val	
180 185 190	
Val Phe His Phe Leu Val Pro Met Ile Ile Val Ile Phe Cys Tyr Leu	
195 200 205	

Arg	Ile	Trp	Ile	Leu	Val	Leu	Gln	Val	Arg	Gln	Arg	Val	Lys	Pro	Asp	
210						215				220						
Arg	Lys	Pro	Lys	Leu	Lys	Pro	Gln	Asp	Phe	Arg	Asn	Phe	Val	Thr	Met	
225				230					235						240	
Phe	Val	Val	Phe	Val	Leu	Phe	Ala	Ile	Cys	Trp	Ala	Pro	Leu	Asn	Phe	
			245						250					255		
Ile	Gly	Leu	Ala	Val	Ala	Ser	Asp	Pro	Ala	Ser	Met	Val	Pro	Arg	Ile	
		260						265					270			
Pro	Glu	Trp	Leu	Phe	Val	Ala	Ser	Tyr	Tyr	Met	Ala	Tyr	Phe	Asn	Ser	
	275						280					285				
Cys	Leu	Asn	Ala	Ile	Ile	Tyr	Gly	Leu	Leu	Asn	Gln	Asn	Phe	Arg	Lys	
290					295					300						
Glu	Tyr	Arg	Arg	Ile	Ile	Val	Ser	Leu	Cys	Thr	Ala	Arg	Val	Phe	Phe	
305				310					315						320	
Val	Asp	Ser	Ser	Asn	Asp	Val	Ala	Asp	Arg	Val	Lys	Trp	Lys	Pro	Ser	
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Met	Lys	Gly	Asn	Val	Ser	Glu	Leu	Leu	Asn	Ala	Thr	Gln	Gln	Ala	Pro	
1				5					10					15		
ggc ggc ggg gag gga ggg aga cca cga ccg tcc tgg atg gcc tct aca																96
Gly	Gly	Gly	Glu	Gly	Gly	Arg	Pro	Arg	Pro	Ser	Trp	Met	Ala	Ser	Thr	
			20					25					30			
ctg gcc ttc atc ctc atc ttt acc atc gtg gtg gac att ctg ggc aac																144
Leu	Ala	Phe	Ile	Leu	Ile	Phe	Thr	Ile	Val	Val	Asp	Ile	Leu	Gly	Asn	
		35					40					45				
ctg ctg gtc atc ctg tct gtg tac cgc aac aag aag ctc agg aac tca																192
Leu	Leu	Val	Ile	Leu	Ser	Val	Tyr	Arg	Asn	Lys	Lys	Leu	Arg	Asn	Ser	
		50				55					60					
ggg aat ata ttt gtg gtg agt tta gct gtg gca gac ctc gtg gtg gct																240
Gly	Asn	Ile	Phe	Val	Val	Ser	Leu	Ala	Val	Ala	Asp	Leu	Val	Val	Ala	
65				70				75						80		
gtt tac cct tat ccc ttg gtg ctg aca tct atc ctt aac aac gga tgg																288
Val	Tyr	Pro	Tyr	Pro	Leu	Val	Leu	Thr	Ser	Ile	Leu	Asn	Asn	Gly	Trp	
			85					90						95		
aat ctg gga tat cta cac tgt caa gtc agc gca ttt cta atg ggc ttg																336
Asn	Leu	Gly	Tyr	Leu	His	Cys	Gln	Val	Ser	Ala	Phe	Leu	Met	Gly	Leu	
			100					105					110			
agt gtc atc ggc tcg ata ttg aac atc acg ggg atc gct atg aac cgt																384
Ser	Val	Ile	Gly	Ser	Ile	Leu	Asn	Ile	Thr	Gly	Ile	Ala	Met	Asn	Arg	
		115					120					125				

tac tgc tac att tgc cac agc ctc aag tac gac aaa ata tac agt aac Tyr Cys Tyr Ile Cys His Ser Leu Lys Tyr Asp Lys Ile Tyr Ser Asn 130 135 140	432
aag aac tcg ctc tgc tac gtg ttc ctg ata tgg atg ctg aca ctc atc Lys Asn Ser Leu Cys Tyr Val Phe Leu Ile Trp Met Leu Thr Leu Ile 145 150 155 160	480
gcc atc atg ccc aac ctg caa acc gga aca ctc cag tac gat ccc cgg Ala Ile Met Pro Asn Leu Gln Thr Gly Thr Leu Gln Tyr Asp Pro Arg 165 170 175	528
atc tac tcc tgt acc ttc acc cag tct gtc agc tca gcg tac acg ata Ile Tyr Ser Cys Thr Phe Thr Gln Ser Val Ser Ser Ala Tyr Thr Ile 180 185 190	576
gca gtg gtg gtt ttc cat ttc atc gtg cct atg att att gtc atc ttc Ala Val Val Val Phe His Phe Ile Val Pro Met Ile Ile Val Ile Phe 195 200 205	624
tgc tac tta agg ata tgg gtc ctg gtc ctt cag gtc aga cgg agg gtg Cys Tyr Leu Arg Ile Trp Val Leu Val Leu Gln Val Arg Arg Arg Val 210 215 220	672
aaa ccc gac aac aag ccc aaa ctg aag ccc cag gac ttc agg aac ttt Lys Pro Asp Asn Lys Pro Lys Leu Lys Pro Gln Asp Phe Arg Asn Phe 225 230 235 240	720
gtc acc atg ttc gta gtt ttt gta ctt ttt gcc att tgt tgg gcc cca Val Thr Met Phe Val Val Phe Val Leu Phe Ala Ile Cys Trp Ala Pro 245 250 255	768
ctc aac ctc ata ggt ctt att gtg gcc tca gac cct gcc acc atg gtc Leu Asn Leu Ile Gly Leu Ile Val Ala Ser Asp Pro Ala Thr Met Val 260 265 270	816
ccc agg atc cca gag tgg ctg ttc gtg gct agt tac tac ctg gcg tac Pro Arg Ile Pro Glu Trp Leu Phe Val Ala Ser Tyr Tyr Leu Ala Tyr 275 280 285	864
ttc aac agc tgc ctc aac gca att ata tac gga cta ctg aat cag aat Phe Asn Ser Cys Leu Asn Ala Ile Ile Tyr Gly Leu Leu Asn Gln Asn 290 295 300	912
ttc aga aag gaa tac aaa aag att att gtc tcg ttg tgc aca gcc aag Phe Arg Lys Glu Tyr Lys Lys Ile Ile Val Ser Leu Cys Thr Ala Lys 305 310 315 320	960
atg ttc ttt gtg gag agt tca aat gaa gaa gca gat aag att aaa tgt Met Phe Phe Val Glu Ser Ser Asn Glu Glu Ala Asp Lys Ile Lys Cys 325 330 335	1008
aag ccc tct cca cta ata ccc aat aat aac ttc ctc ccg gtg gac tct Lys Pro Ser Pro Leu Ile Pro Asn Asn Asn Phe Leu Pro Val Asp Ser 340 345 350	1056
gtt taa Val	1062

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 Leu Ala Phe Ile Leu Ile Phe Thr Ile Val Val Asp Ile Leu Gly Asn
 35 40 45
 Leu Leu Val Ile Leu Ser Val Tyr Arg Asn Lys Lys Leu Arg Asn Ser
 50 55 60
 Gly Asn Ile Phe Val Val Ser Leu Ala Val Ala Asp Leu Val Val Ala
 65 70 75 80
 Val Tyr Pro Tyr Pro Leu Val Leu Thr Ser Ile Leu Asn Asn Gly Trp
 85 90 95
 Asn Leu Gly Tyr Leu His Cys Gln Val Ser Ala Phe Leu Met Gly Leu
 100 105 110
 Ser Val Ile Gly Ser Ile Leu Asn Ile Thr Gly Ile Ala Met Asn Arg
 115 120 125
 Tyr Cys Tyr Ile Cys His Ser Leu Lys Tyr Asp Lys Ile Tyr Ser Asn
 130 135 140
 Lys Asn Ser Leu Cys Tyr Val Phe Leu Ile Trp Met Leu Thr Leu Ile
 145 150 155 160
 Ala Ile Met Pro Asn Leu Gln Thr Gly Thr Leu Gln Tyr Asp Pro Arg
 165 170 175
 Ile Tyr Ser Cys Thr Phe Thr Gln Ser Val Ser Ser Ala Tyr Thr Ile
 180 185 190
 Ala Val Val Val Phe His Phe Ile Val Pro Met Ile Ile Val Ile Phe
 195 200 205
 Cys Tyr Leu Arg Ile Trp Val Leu Val Leu Gln Val Arg Arg Arg Val
 210 215 220
 Lys Pro Asp Asn Lys Pro Lys Leu Lys Pro Gln Asp Phe Arg Asn Phe
 225 230 235 240
 Val Thr Met Phe Val Val Phe Val Leu Phe Ala Ile Cys Trp Ala Pro
 245 250 255
 Leu Asn Leu Ile Gly Leu Ile Val Ala Ser Asp Pro Ala Thr Met Val
 260 265 270
 Pro Arg Ile Pro Glu Trp Leu Phe Val Ala Ser Tyr Tyr Leu Ala Tyr
 275 280 285
 Phe Asn Ser Cys Leu Asn Ala Ile Ile Tyr Gly Leu Leu Asn Gln Asn
 290 295 300
 Phe Arg Lys Glu Tyr Lys Lys Ile Ile Val Ser Leu Cys Thr Ala Lys
 305 310 315 320
 Met Phe Phe Val Glu Ser Ser Asn Glu Glu Ala Asp Lys Ile Lys Cys
 325 330 335
 Lys Pro Ser Pro Leu Ile Pro Asn Asn Asn Phe Leu Pro Val Asp Ser
 340 345 350
 Val

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (13)...(1098)

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	Met	Ser	Glu	Asn	Gly	Ser	Phe	Ala	Asn	Cys	Cys	Glu	Ala		
	1				5					10					
ggc	ggg	tgg	gca	gtg	cgc	ccg	ggc	tgg	tgc	ggg	gct	ggc	agc	gcg	99
Gly	Gly	Trp	Ala	Val	Arg	Pro	Gly	Trp	Ser	Gly	Ala	Gly	Ser	Ala	
	15					20					25				
ccc	tcc	agg	acc	cct	cga	cct	ccc	tgg	gtg	gct	cca	gcg	ctg	tcc	147
Pro	Ser	Arg	Thr	Pro	Arg	Pro	Pro	Trp	Val	Ala	Pro	Ala	Leu	Ser	
	30				35					40				45	
gtg	ctc	atc	gtc	acc	acc	gcc	gtg	gac	gtc	gtg	ggc	aac	ctc	ctg	195
Val	Leu	Ile	Val	Thr	Thr	Ala	Val	Asp	Val	Val	Gly	Asn	Leu	Leu	
				50				55					60		
atc	ctc	tcc	gtg	ctc	agg	aac	cgc	aag	ctc	cgg	aac	gca	ggt	aat	243
Ile	Leu	Ser	Val	Leu	Arg	Asn	Arg	Lys	Leu	Arg	Asn	Ala	Gly	Asn	
			65					70					75		
ttc	ttg	gtg	agt	ctg	gca	ttg	gct	gac	ctg	gtg	gtg	gcc	ttc	tac	291
Phe	Leu	Val	Ser	Leu	Ala	Leu	Ala	Asp	Leu	Val	Val	Ala	Phe	Tyr	
		80					85					90			
tac	ccg	cta	atc	ctc	gtg	gcc	atc	ttc	tat	gac	ggc	tgg	gcc	ctg	339
Tyr	Pro	Leu	Ile	Leu	Val	Ala	Ile	Phe	Tyr	Asp	Gly	Trp	Ala	Leu	
	95					100					105				
gag	gag	cac	tgc	aag	gcc	agc	gcc	ttt	gtg	atg	ggc	ctg	agc	gtc	387
Glu	Glu	His	Cys	Lys	Ala	Ser	Ala	Phe	Val	Met	Gly	Leu	Ser	Val	
	110				115					120				125	
ggc	tct	gtc	ttc	aat	atc	act	gcc	atc	gcc	att	aac	cgc	tac	tgc	435
Gly	Ser	Val	Phe	Asn	Ile	Thr	Ala	Ile	Ala	Ile	Asn	Arg	Tyr	Cys	
				130					135					140	
atc	tgc	cac	agc	atg	gcc	tac	cac	cga	atc	tac	cgg	cgc	tgg	cac	483
Ile	Cys	His	Ser	Met	Ala	Tyr	His	Arg	Ile	Tyr	Arg	Arg	Trp	His	
			145					150					155		
cct	ctg	cac	atc	tgc	ctc	atc	tgg	ctc	ctc	acc	gtg	gtg	gcc	ttg	531
Pro	Leu	His	Ile	Cys	Leu	Ile	Trp	Leu	Leu	Thr	Val	Val	Ala	Leu	
		160					165					170			
ccc	aac	ttc	ttt	gtg	ggg	tcc	ctg	gag	tac	gac	cca	cgc	atc	tat	579
Pro	Asn	Phe	Phe	Val	Gly	Ser	Leu	Glu	Tyr	Asp	Pro	Arg	Ile	Tyr	
	175					180					185				
tgc	acc	ttc	atc	cag	acc	gcc	agc	acc	cag	tac	acg	gcg	gca	gtg	627
Cys	Thr	Phe	Ile	Gln	Thr	Ala	Ser	Thr	Gln	Tyr	Thr	Ala	Ala	Val	
	190				195					200				205	
gtc	atc	cac	ttc	ctc	ctc	cct	atc	gct	gtc	gtg	tcc	ttc	tgc	tac	675
Val	Ile	His	Phe	Leu	Leu	Pro	Ile	Ala	Val	Val	Ser	Phe	Cys	Tyr	
				210					215					220	
cgc	atc	tgg	gtg	ctg	gtg	ctt	cag	gcc	cgc	agg	aaa	gcc	aag	cca	723
Arg	Ile	Trp	Val	Leu	Val	Leu	Gln	Ala	Arg	Arg	Lys	Ala	Lys	Pro	
			225					230					235		

agc agg ctg tgc ctg aag ccc agc gac ttg cgg agc ttt cta acc atg	771
Ser Arg Leu Cys Leu Lys Pro Ser Asp Leu Arg Ser Phe Leu Thr Met	
240 245 250	
ttt gtg gtg ttt gtg atc ttt gcc atc tgc tgg gct cca ctt aac tgc	819
Phe Val Val Phe Val Ile Phe Ala Ile Cys Trp Ala Pro Leu Asn Cys	
255 260 265	
atc ggc ctc gct gtg gcc atc aac ccc caa gaa atg gct ccc cag atc	867
Ile Gly Leu Ala Val Ala Ile Asn Pro Gln Glu Met Ala Pro Gln Ile	
270 275 280 285	
cct gag ggg cta ttt gtc act agc tac tta ctg gct tat ttc aac agc	915
Pro Glu Gly Leu Phe Val Thr Ser Tyr Leu Leu Ala Tyr Phe Asn Ser	
290 295 300	
tgc ctg aat gcc att gtc tat ggg ctc ttg aac caa aac ttc cgc agg	963
Cys Leu Asn Ala Ile Val Tyr Gly Leu Leu Asn Gln Asn Phe Arg Arg	
305 310 315	
gaa tac aag agg atc ctc ttg gcc ctt tgg aac cca cgg cac tgc att	1011
Glu Tyr Lys Arg Ile Leu Leu Ala Leu Trp Asn Pro Arg His Cys Ile	
320 325 330	
caa gat gct tcc aag ggc agc cac gcg gag ggg ctg cag agc cca gct	1059
Gln Asp Ala Ser Lys Gly Ser His Ala Glu Gly Leu Gln Ser Pro Ala	
335 340 345	
cca ccc atc att ggt gtg cag cac cag gca gat gct ctc tagcctg	1105
Pro Pro Ile Ile Gly Val Gln His Gln Ala Asp Ala Leu	
350 355 360	

<210> 16
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<400> 16

Met Ser Glu Asn Gly Ser Phe Ala Asn Cys Cys Glu Ala Gly Gly Trp	
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Thr Pro Arg Pro Pro Trp Val Ala Pro Ala Leu Ser Ala Val Leu Ile	
35 40 45	
Val Thr Thr Ala Val Asp Val Val Gly Asn Leu Leu Val Ile Leu Ser	
50 55 60	
Val Leu Arg Asn Arg Lys Leu Arg Asn Ala Gly Asn Leu Phe Leu Val	
65 70 75 80	
Ser Leu Ala Leu Ala Asp Leu Val Val Ala Phe Tyr Pro Tyr Pro Leu	
85 90 95	
Ile Leu Val Ala Ile Phe Tyr Asp Gly Trp Ala Leu Gly Glu Glu His	
100 105 110	
Cys Lys Ala Ser Ala Phe Val Met Gly Leu Ser Val Ile Gly Ser Val	
115 120 125	
Phe Asn Ile Thr Ala Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys His	
130 135 140	
Ser Met Ala Tyr His Arg Ile Tyr Arg Arg Trp His Thr Pro Leu His	
145 150 155 160	
Ile Cys Leu Ile Trp Leu Leu Thr Val Val Ala Leu Leu Pro Asn Phe	
165 170 175	

Phe	Val	Gly	Ser	Leu	Glu	Tyr	Asp	Pro	Arg	Ile	Tyr	Ser	Cys	Thr	Phe
			180					185					190		
Ile	Gln	Thr	Ala	Ser	Thr	Gln	Tyr	Thr	Ala	Ala	Val	Val	Val	Ile	His
			195				200					205			
Phe	Leu	Leu	Pro	Ile	Ala	Val	Val	Ser	Phe	Cys	Tyr	Leu	Arg	Ile	Trp
	210					215					220				
Val	Leu	Val	Leu	Gln	Ala	Arg	Arg	Lys	Ala	Lys	Pro	Glu	Ser	Arg	Leu
225				230						235					240
Cys	Leu	Lys	Pro	Ser	Asp	Leu	Arg	Ser	Phe	Leu	Thr	Met	Phe	Val	Val
			245						250					255	
Phe	Val	Ile	Phe	Ala	Ile	Cys	Trp	Ala	Pro	Leu	Asn	Cys	Ile	Gly	Leu
			260					265					270		
Ala	Val	Ala	Ile	Asn	Pro	Gln	Glu	Met	Ala	Pro	Gln	Ile	Pro	Glu	Gly
	275					280						285			
Leu	Phe	Val	Thr	Ser	Tyr	Leu	Leu	Ala	Tyr	Phe	Asn	Ser	Cys	Leu	Asn
	290					295					300				
Ala	Ile	Val	Tyr	Gly	Leu	Leu	Asn	Gln	Asn	Phe	Arg	Arg	Glu	Tyr	Lys
305				310						315					320
Arg	Ile	Leu	Leu	Ala	Leu	Trp	Asn	Pro	Arg	His	Cys	Ile	Gln	Asp	Ala
			325					330						335	
Ser	Lys	Gly	Ser	His	Ala	Glu	Gly	Leu	Gln	Ser	Pro	Ala	Pro	Pro	Ile
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 1 5

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<400> 18
 Cys Tyr Ile Cys His Ser
 1 5

<210> 19
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27

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<210> 23 <211> 24 <212> DNA <213> Homo sapiens	
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<210> 24 <211> 21 <212> DNA <213> Homo sapiens	
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cactgaactt ctgattcgca aactt	25
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